

SEQUENCE LISTING

(1) GENERAL INFORMATION

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(ii) TITLE OF THE INVENTION: ANTICOAGULANT AGENTS USEFUL IN TREATMENT
OF THROMBOSIS

(iii) NUMBER OF SEQUENCES: 111

(iv) CORRESPONDENCE ADDRESS:

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(D) STATE: PA
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(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Diskette
(B) COMPUTER: IBM Compatible
(C) OPERATING SYSTEM: DOS
(D) SOFTWARE: FastSEQ Version 1.5

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:
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(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 60/029,119
(B) FILING DATE: 24-OCT-1996

(viii) ATTORNEY/AGENT INFORMATION:

- (A) NAME: Baumeister, Kirk
- (B) REGISTRATION NUMBER: 33,833
- (C) REFERENCE/DOCKET NUMBER: P50438

(ix) TELECOMMUNICATION INFORMATION:

- (A) TELEPHONE: 610-270-5096
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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CATCCTAGAG TCACCGAGGA

20

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

AGCTGCCCAA AGTGCCAAG C

21

- (2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 36 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CTAACACTCA TTCCTGTTGA AGCTCTTGAC AATGGG

36

- (2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GATTTTCARG TGCAGATTT C

21

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 363 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CAGATCCAGT	TGGTGCAGTC	TGGACCTGAG	CTGAAGAACG	CTGGAGAGAC	AGTCAAGATC	60
TCCTGCAGG	CTTCTGGGTA	CACCTTCACA	AACTATGGAA	TGAACTGGGT	GAAGCAGGCT	120
CCAGGAAAGG	GTAAACACCA	GAAATGGAAA	GTCAACATAT			180
GTTGATGACT	TCAAGGGACG	GTTCGCCTTC	TCTTTGGAAA	GCTCTGCCAG	CACTGCCAAT	240
TTGCAGATCG	ACAACCTCAA	AGATGAGGAC	ACGGCTACAT	ATTCTGTAC	AAGAGAAGGG	300
AATATGGATG	GTAACTTCCC	TTTTACTTAC	TGGGGCCAAG	GGACTCTGGT	CACTGTCTCT	360
GCA						363

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 321 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

CAAATTGTTC	TCTCCCAGTC	TCCAGCAATC	CTGTCTGCAT	CTCCAGGGGA	GAAGGTCACA	60
ATGACTTGCA	GGGCCAGCTC	AAGTGTAAAT	TACATGCACT	GGTACCAGCA	GAAGCCAGGA	120
TCCTCCCCCA	AACCCTGGAT	TTATGCCACA	TCCAACCTGG	CTTCTGGAGT	CCCTGCTCGC	180
TTCAGTGGCA	GTGGGTCTGG	GACCTCTTAC	TCTCTCACAA	TCAGCAGAGT	GGAGGCTGAA	240
GATGCTGCCA	CTTATTACTG	CCAGCAGTGG	AGTATTAACC	CACGGACGTT	CGGTGGAGGC	300
ACCAAGCTGG	AAATCAAACG	G				321

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 121 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE: internal
- (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Gln	Ile	Gln	Leu	Val	Gln	Ser	Gly	Pro	Glu	Leu	Lys	Lys	Pro	Gly	Glu
1					5				10					15	
Thr	Val	Lys	Ile	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Phe	Thr	Asn	Tyr
									20			25		30	
Gly	Met	Asn	Trp	Val	Lys	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Lys	Trp	Met
					35			40				45			
Gly	Trp	Ile	Asn	Thr	Arg	Asn	Gly	Lys	Ser	Thr	Tyr	Val	Asp	Asp	Phe
					50			55			60				
Lys	Gly	Arg	Phe	Ala	Phe	Ser	Leu	Glu	Ser	Ser	Ala	Ser	Thr	Ala	Asn
					65			70			75		80		
Leu	Gln	Ile	Asp	Asn	Leu	Lys	Asp	Glu	Asp	Thr	Ala	Thr	Tyr	Phe	Cys
					85				90			95			
Thr	Arg	Glu	Gly	Asn	Met	Asp	Gly	Tyr	Phe	Pro	Phe	Thr	Tyr	Trp	Gly
					100			105			110				
Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ala							
					115			120							

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Asn Tyr Gly Met Asn

1 5

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Trp Ile Asn Thr Arg Asn Gly Lys Ser Thr Tyr Val Asp Asp Phe Lys

1 5 10 15

Gly

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Glu	Gly	Asn	Met	Asp	Gly	Tyr	Phe	Pro	Phe	Thr	Tyr
1											
			5							10	

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Gln	Ile	Val	Leu	Ser	Gln	Ser	Pro	Ala	Ile	Leu	Ser	Ala	Ser	Pro	Gly
1															15
			5							10					
Glu	Lys	Val	Thr	Met	Thr	Cys	Arg	Ala	Ser	Ser	Ser	Val	Asn	Tyr	Met
			20							25				30	
His	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Ser	Ser	Pro	Lys	Pro	Trp	Ile	Tyr
			35					40					45		

Ala Thr Ser Asn Leu Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser
 50 55 60
 Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Arg Val Glu Ala Glu
 65 70 75 80
 Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ile Asn Pro Arg Thr
 85 90 95
 Phe Gly Gly Thr Lys Leu Glu Ile Lys Arg
 100 105

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE: internal
- (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Arg Ala Ser Ser Ser Val Asn Tyr Met His
 1 5 10

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE: internal
- (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Ala Thr Ser Asn Leu Ala Ser
1 5

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE: internal
- (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Gln Gln Trp Ser Ile Asn Pro Arg Thr
1 5

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

CAACTAGTGC AATCTGGGTC TGAGTTGAAG AAGCCTGGGG CCTCAGTGAA GGTTTCCTGC 60
AAGGCCTCTG GATACACCTT CACTAACTAT GGAATGAACT GGGT 104

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 108 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

TTGAAGTCAT CAACATATGT TGACTTCCA TTTCTGGTGT TTATCCATCC CATCCACTCG	60
AGCCCTTGTC CAGGGGCCTG TCGCACCCAG TTCATTCCAT AGTTAGTG	108

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GTCAACATAT GTTGATGACT TCAAGGGCG GTTTGTCTTC CCTCTGTCAG CACGGCATAT	60
CTACAGATCA GCAGCCTAAA GGCTGACGAC ACTGCAGTGT ATTACTG	107

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 91 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

GGTACCCTGG CCCCAGTAAG TAAAAGGGAA GTAACCATCC ATATTCCCTT CTCTCGCACA	60
GTAATACACT GCAGTGTGCGT CAGCCTTTAG G	91

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 337 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence

(B) LOCATION: 2...337

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

A CTA GTG CAA TCT GGG TCT GAG TTG AAG AAG CCT GGG GCC TCA GTG AAG	49
Leu Val Gln Ser Gly Ser Glu Leu Lys Lys Pro Gly Ala Ser Val Lys	
1 5 10 15	
GT TCC TGC AAG GCC TCT GGA TAC ACC TTC ACT AAC TAT GGA ATG AAC	97
Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn Tyr Gly Met Asn	
20 25 30	
TGG GTG CGA CAG GCC CCT GGA CAA GGG CTC GAG TGG ATG GGA TGG ATA	145
Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly Trp Ile	
35 40 45	
AAC ACC AGA AAT GGA AAG TCA ACA TAT GTT GAT GAC TTC AAG GGG CGG	193
Asn Thr Arg Asn Gly Lys Ser Thr Tyr Val Asp Asp Phe Lys Gly Arg	
50 55 60	
TTT GTC TTC TCC TTG GAC ACC TCT GTC AGC ACG GCA TAT CTA CAG ATC	241
Phe Val Phe Ser Leu Asp Thr Ser Val Ser Thr Ala Tyr Leu Gln Ile	
65 70 75 80	
AGC AGC CTA AAG GCT GAC GAC ACT GCA GTG TAT TAC TGT GCG AGA GAA	289
Ser Ser Leu Lys Ala Asp Asp Thr Ala Val Tyr Tyr Cys Ala Arg Glu	
85 90 95	
GGG AAT ATG GAT GGT TAC TTC CCT TTT ACT TAC TGG GGC CAG GGT ACC	337
Gly Asn Met Asp Gly Tyr Phe Pro Phe Thr Tyr Trp Gly Gln Gly Thr	
100 105 110	

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 112 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Leu	Val	Gln	Ser	Gly	Ser	Glu	Leu	Lys	Lys	Pro	Gly	Ala	Ser	Val	Lys
1						5			10					15	
Val	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Phe	Thr	Asn	Tyr	Gly	Met	Asn
							20		25				30		
Trp	Val	Arg	Gln	Ala	Pro	Gly	Gln	Gly	Leu	Glu	Trp	Met	Gly	Trp	Ile
									40				45		
Asn	Thr	Arg	Asn	Gly	Lys	Ser	Thr	Tyr	Val	Asp	Asp	Phe	Lys	Gly	Arg
						50			55			60			
Phe	Val	Phe	Ser	Leu	Asp	Thr	Ser	Val	Ser	Thr	Ala	Tyr	Leu	Gln	Ile
						65			70			75		80	
Ser	Ser	Leu	Lys	Ala	Asp	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	Ala	Arg	Glu
							85			90			95		
Gly	Asn	Met	Asp	Gly	Tyr	Phe	Pro	Phe	Thr	Tyr	Trp	Gly	Gln	Gly	Thr
						100			105			110			

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

GCTACTAGTG CAATCTGGGT CTGAGTTGAA GCC

33

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

TGGGTACCTT GGCCCCAGTA AGTAAAAGGG

30

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 97 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:
- (ix) FEATURE:
 - (A) NAME/KEY: Coding Sequence
 - (B) LOCATION: 27...95
 - (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

GAATTCTGAG CACACAGGAC CTCACC ATG GGA TGG AGC TGT ATC ATC CTC TTC
 Met Gly Trp Ser Cys Ile Ile Leu Phe

1

5

53

TTG GTA GCA ACA GCA GGT GTC CAC TCC CAG GTC CAA CTA GT
 Leu Val Ala Thr Ala Thr Gly Val His Ser Gln Val Gln Leu
 10 15 20

97

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly
 1 5 10 15
 Val His Ser Gln Val Gln Leu
 20

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 110 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

GGAGACGCCA TCGAATTCTG AGCACACAGG ACCTCACCAT GGGATGGAGC TGTATCATCC	60
TCTTCTTGGT AGCAACAGCT ACAGGTGTCC ACTCCCAGGT CCAACTGCAG	110

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

GGAGACGCCA TCGAATTCTG A	21
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(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

GATTGCACTA GTTGGACCTG GGAGTGGACA	30
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(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 77 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

CTAGAGTGGG TCGCAGAGAT CTCTGATGGT GGTAGTTACA CCTACTATCC AGACACTGTG	60
ACGGGCCGGT TCACGAT	77

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 73 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

ATCGTGAACC GGCCCGTCAC AGTGTCTGGA TAGTAGGTGT AACTACCACC ATCAGAGATC	60
TCTGCGACCC ACT	73

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 363 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence

(B) LOCATION: 1...363

(D) OTHER INFORMATION: F9HZHC 1-0

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

CAG GTG CAA CTA GTG CAA TCT GGG TCT GAG TTG AAG AAG CCT GGG GCC	48
Gln Val Gln Leu Val Gln Ser Gly Ser Glu Leu Lys Lys Pro Gly Ala	
1 5 10 15	
TCA GTG AAG GTT TCC TGC AAG GCC TCT GGA TAC ACC TTC ACT AAC TAT	96
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn Tyr	
20 25 30	
GGA ATG AAC TGG GTG CGA CAG GCC CCT GGA CAA GGG CTC GAG TGG ATG	144
Gly Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met	
35 40 45	
GGA TGG ATA AAC ACC AGA AAT GGA AAG TCA ACA TAT GTT GAT GAC TTC	192
Gly Trp Ile Asn Thr Arg Asn Gly Lys Ser Thr Tyr Val Asp Asp Phe	
50 55 60	
AAG GGA CGG TTT GTC TTC TCC TTG GAC ACC TCT GTC AGC ACG GCA TAT	240
Lys Gly Arg Phe Val Phe Ser Leu Asp Thr Ser Val Ser Thr Ala Tyr	
65 70 75 80	

CTA CAG ATC AGC AGC CTA AAG GCT GAC GAC ACT GCA GTG TAT TAC TGT	288	
Leu Gln Ile Ser Ser Leu Lys Ala Asp Asp Thr Ala Val Tyr Tyr Cys		
85	90	95
GCG AGA GAA GGG AAT ATG GAT GGT TAC TTC CCT TTT ACT TAC TGG GGC	336	
Ala Arg Glu Gly Asn Met Asp Gly Tyr Phe Pro Phe Thr Tyr Trp Gly		
100	105	110
CAG GGT ACC CTG GTC ACC GTC TCC TCA	363	
Gln Gly Thr Leu Val Thr Val Ser Ser		
115	120	

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 121 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

Gln Val Gln Leu Val Gln Ser Gly Ser Glu Leu Lys Lys Pro Gly Ala			
1	5	10	15
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn Tyr			
20	25	30	
Gly Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met			
35	40	45	
Gly Trp Ile Asn Thr Arg Asn Gly Lys Ser Thr Tyr Val Asp Asp Phe			
50	55	60	
Lys Gly Arg Phe Val Phe Ser Leu Asp Thr Ser Val Ser Thr Ala Tyr			
65	70	75	80
Leu Gln Ile Ser Ser Leu Lys Ala Asp Asp Thr Ala Val Tyr Tyr Cys			
85	90	95	
Ala Arg Glu Gly Asn Met Asp Gly Tyr Phe Pro Phe Thr Tyr Trp Gly			
100	105	110	

Gln Gly Thr Leu Val Thr Val Ser Ser
 115 120

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 165 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

AGTACTGACA CAGTCTCCAG CCACCCCTGTC TTTGTCTCCA GGGGAAAGAG CCACCCCTCTC	60
CTGCAGGGCC AGCTCAAGTG TAAATTACAT GCACTGGTAC CAACAGAGAC CTGGCCAGGC	120
TCCCAGGCTC CTCATCTATG CCACTAGTAA CCTGGCTTCT GGCAT	165

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 146 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

CCGCGGGTTA ATACTCCACT GCTGACAGTA ATAAACCGCA AAATCTTCAG GCTCTAGACT	60
GCTGATGGTG AGAGTGAAAT CTGTCCCAGA CCCGGATCCA CTGAACCTGG CTGGGATGCC	120
AGAAGGCCAGG TTACTAGTGG CATAGA	146

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 280 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence

(B) LOCATION: 2...280

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

A	GTA	CTG	ACA	CAG	TCT	CCA	GCC	ACC	CTG	TCT	TTG	TCT	CCA	GGG	GAA	AGA	49
Val	Leu	Thr	Gln	Ser	Pro	Ala	Thr	Leu	Ser	Leu	Ser	Pro	Gly	Glu	Arg		
1	5							10						15			
GCC	ACC	CTC	TCC	TGC	AGG	GCC	AGC	TCA	AGT	GTA	AAT	TAC	ATG	CAC	TGG	97	
Ala	Thr	Leu	Ser	Cys	Arg	Ala	Ser	Ser	Ser	Val	Asn	Tyr	Met	His	Trp		
20	25													30			
TAC	CAA	CAG	AGA	CCT	GGC	CAG	GCT	CCC	AGG	CTC	CTC	ATC	TAT	GCC	ACT	145	
Tyr	Gln	Gln	Arg	Pro	Gly	Gln	Ala	Pro	Arg	Leu	Leu	Ile	Tyr	Ala	Thr		
35	40													45			
AGT	AAC	CTG	GCT	TCT	GGC	ATC	CCA	GCC	AGG	TTC	AGT	GGA	TCC	GGG	TCT	193	
Ser	Asn	Leu	Ala	Ser	Gly	Ile	Pro	Ala	Arg	Phe	Ser	Gly	Ser	Gly	Ser		
50	55													60			
GGG	ACA	GAT	TTC	ACT	CTC	ACC	ATC	AGC	AGT	CTA	GAG	CCT	GAA	GAT	TTT	241	
Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile	Ser	Ser	Leu	Glu	Pro	Glu	Asp	Phe		
65	70													80			

280

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 93 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

TCGAGTACTG ACACAGTCTC CAGCCAC

27

(2) INFORMATION FOR SEQ ID NO:37:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

GACCGCGGGT TAATACTCCA CTGCTGA

27

(2) INFORMATION FOR SEQ ID NO:38:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 94 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:
- (ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 27...92
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

GAATTCTGAG CACACAGGAC CTCACC ATG GGA TGG AGC TGT ATC ATC CTC TTC	53
Met Gly Trp Ser Cys Ile Ile Leu Phe	
1	5

TTG GTA GCA ACA GCT ACA GGT GTC CAC TCC GAG ATA GTA CT	94
Leu Val Ala Thr Ala Thr Gly Val His Ser Glu Ile Val	
10	15
	20

(2) INFORMATION FOR SEQ ID NO:39:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE: internal
- (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly	
1	5
Val His Ser Glu Ile Val	15
20	

(2) INFORMATION FOR SEQ ID NO:40:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

GACTGTGTCA GTACTATCTC GGAGTGGACA

30

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 55 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

GGGCAGCCTC CTAAGTTGCT CATTACTGG GCGTCGACTA GGAAATCTGG GGTAC

55

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 51 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

CCCAAGATTCC CTAGTCGACG CCCAGTAAAT GAGCAACTTA GGAGGCTGCC C

51

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 321 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

 (ii) MOLECULE TYPE: cDNA
 (iii) HYPOTHETICAL: NO
 (iv) ANTISENSE: NO
 (v) FRAGMENT TYPE:
 (vi) ORIGINAL SOURCE:
 (ix) FEATURE:

 (A) NAME/KEY: Coding Sequence
 (B) LOCATION: 1...321
 (D) OTHER INFORMATION: F9HZLC1-0

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

GAA ATA GTA CTG ACA CAG TCT CCA GCC ACC CTG TCT TTG TCT CCA GGG
 Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
 1 5 10 15

48

GAA AGA GCC ACC CTC TCC TGC AGG GCC AGC TCA AGT GTA AAT TAC ATG
 Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Ser Ser Val Asn Tyr Met
 20 25 30

96

CAC TGG TAC CAA CAG AGA CCT GGC CAG GCT CCC AGG CTC CTC ATC TAT
 His Trp Tyr Gln Gln Arg Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr
 35 40 45

144

GCC ACT AGT AAC CTG GCT TCT GGC ATC CCA GCC AGG TTC AGT GGA TCC	192		
Ala Thr Ser Asn Leu Ala Ser Gly Ile Pro Ala Arg Phe Ser Gly Ser			
50	55	60	
GGG TCT GGG ACA GAT TTC ACT CTC ACC ATC AGC AGT CTA GAG CCT GAA	240		
Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro Glu			
65	70	75	80
GAT TTT GCG GTT TAT TAC TGT CAG CAG TGG AGT ATT AAC CCG CGG ACG	288		
Asp Phe Ala Val Tyr Tyr Cys Gln Gln Trp Ser Ile Asn Pro Arg Thr			
85	90	95	
TTC GGC GGA GGG ACC AAG GTG GAG ATC AAA CGA	321		
Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg			
100	105		

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly			
1	5	10	15
Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Ser Ser Val Asn Tyr Met			
20	25	30	
His Trp Tyr Gln Gln Arg Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr			
35	40	45	
Ala Thr Ser Asn Leu Ala Ser Gly Ile Pro Ala Arg Phe Ser Gly Ser			
50	55	60	
Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro Glu			
65	70	75	80

Asp	Phe	Ala	Val	Tyr	Tyr	Cys	Gln	Gln	Trp	Ser	Ile	Asn	Pro	Arg	Thr
														85	90
															95
Phe	Gly	Gly	Gly	Thr	Lys	Val	Glu	Ile	Lys	Arg					
														100	105

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 134 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

CCTGGACAAG	GGCTCAAGTG	GATGGGATGG	ATAAACACCA	GAAATGGAAA	GTCAACATAT	60
GTTGATGACT	TCAAGGGACG	GTTCGTCTTC	TCTCTAGACT	CCTCTGTCAG	CACGGCATAT	120
CTACAGATCA	GCAG					134

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 134 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

GGTACCCCTGG CCCCAGTAAG TAAAAGGGAA GTAACCATCC ATATTCCCTT CTCTCGTACA	60
GTAATACACT GCAGTGTGCGT CAGCCTTAG GCTGCTGATC TGTAGATATG CCGTGCTGAC	120
AGAGGAGTCT AGAG	134

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 225 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence

(B) LOCATION: 1...225

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

CCT GGA CAA GGG CTC AAG TGG ATG GGA TGG ATA AAC ACC ACC AGA AAT GGA	48		
Pro Gly Gln Gly Leu Lys Trp Met Gly Trp Ile Asn Thr Arg Asn Gly			
1	5	10	15

AAG TCA ACA TAT GTT GAT GAC TTC AAG GGA CGG TTT GTC TTC TCT CTA	96		
Lys Ser Thr Tyr Val Asp Asp Phe Lys Gly Arg Phe Val Phe Ser Leu			
20	25	30	

GAC TCC TCT GTC AGC ACG GCA TAT CTA CAG ATC AGC AGC CTA AAG GCT	144		
Asp Ser Ser Val Ser Thr Ala Tyr Leu Gln Ile Ser Ser Leu Lys Ala			
35	40	45	

GAC GAC ACT GCA GTG TAT TAC TGT ACG AGA GAA GGG AAT ATG GAT GGT	192	
Asp Asp Thr Ala Val Tyr Tyr Cys Thr Arg Glu Gly Asn Met Asp Gly		
50	55	60

TAC TTC CCT TTT ACT TAC TGG GGC CAG GGT ACC	225	
Tyr Phe Pro Phe Thr Tyr Trp Gly Gln Gly Thr		
65	70	75

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 75 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE: internal
- (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

Pro Gly Gln Gly Leu Lys Trp Met Gly Trp Ile Asn Thr Arg Asn Gly			
1	5	10	15
Lys Ser Thr Tyr Val Asp Asp Phe Lys Gly Arg Phe Val Phe Ser Leu			
20	25	30	
Asp Ser Ser Val Ser Thr Ala Tyr Leu Gln Ile Ser Ser Leu Lys Ala			
35	40	45	
Asp Asp Thr Ala Val Tyr Tyr Cys Thr Arg Glu Gly Asn Met Asp Gly			
50	55	60	
Tyr Phe Pro Phe Thr Tyr Trp Gly Gln Gly Thr			
65	70	75	

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

TTTCCTGGAC AAGGGCTCAA GTGGATG

27

(2) INFORMATION FOR SEQ ID NO:50:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

TTTGGTACCC TGGCCCCAGT AAGT

24

(2) INFORMATION FOR SEQ ID NO:51:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 363 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 1...363
- (D) OTHER INFORMATION: F9HZHC 1-1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

CAG GTG CAA CTA GTG CAA TCT GGG TCT GAG TTG AAG AAG CCT GGG GCC	48
Gln Val Gln Leu Val Gln Ser Gly Ser Glu Leu Lys Lys Pro Gly Ala	
1 5 10 15	
TCA GTG AAG GTT TCC TGC AAG GCC TCT GGA TAC ACC TTC ACT AAC TAT	96
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn Tyr	
20 25 30	
GGA ATG AAC TGG GTG CGA CAG GCC CCT GGA CAA GGG CTC AAG TGG ATG	144
Gly Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Lys Trp Met	
35 40 45	
GGA TGG ATA AAC ACC AGA AAT GGA AAG TCA ACA TAT GTT GAT GAC TTC	192
Gly Trp Ile Asn Thr Arg Asn Gly Lys Ser Thr Tyr Val Asp Asp Phe	
50 55 60	
AAG GGA CGG TTT GTC TTC TCT CTA GAC TCC TCT GTC AGC ACG GCA TAT	240
Lys Gly Arg Phe Val Phe Ser Leu Asp Ser Ser Val Ser Thr Ala Tyr	
65 70 75 80	
CTA CAG ATC AGC AGC CTA AAG GCT GAC GAC ACT GCA GTG TAT TAC TGT	288
Leu Gln Ile Ser Ser Leu Lys Ala Asp Asp Thr Ala Val Tyr Tyr Cys	
85 90 95	
ACG AGA GAA GGG AAT ATG GAT GGT TAC TTC CCT TTT ACT TAC TGG GGC	336
Thr Arg Glu Gly Asn Met Asp Gly Tyr Phe Pro Phe Thr Tyr Trp Gly	
100 105 110	
CAG GGT ACC CTG GTC ACC GTC TCC TCA	363
Gln Gly Thr Leu Val Thr Val Ser Ser	
115 120	

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 121 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

Gln	Val	Gln	Leu	Val	Gln	Ser	Gly	Ser	Glu	Leu	Lys	Lys	Pro	Gly	Ala
1				5					10					15	
Ser	Val	Lys	Val	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Phe	Thr	Asn	Tyr
									20			25		30	
Gly	Met	Asn	Trp	Val	Arg	Gln	Ala	Pro	Gly	Gln	Gly	Leu	Lys	Trp	Met
									35			40		45	
Gly	Trp	Ile	Asn	Thr	Arg	Asn	Gly	Lys	Ser	Thr	Tyr	Val	Asp	Asp	Phe
									50			55		60	
Lys	Gly	Arg	Phe	Val	Phe	Ser	Leu	Asp	Ser	Ser	Val	Ser	Thr	Ala	Tyr
									65			70		75	
Leu	Gln	Ile	Ser	Ser	Leu	Lys	Ala	Asp	Asp	Thr	Ala	Val	Tyr	Tyr	Cys
									85			90		95	
Thr	Arg	Glu	Gly	Asn	Met	Asp	Gly	Tyr	Phe	Pro	Phe	Thr	Tyr	Trp	Gly
									100			105		110	
Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser							
									115			120			

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 82 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

CAACAGAGAC CTGGCCAGGC TCCCAAGCCC TGGATCTATG CCACGAGTAA CCTGGCTAGC	60
GGCGTCCCAG CCAGGTTCAAG TG	82

(2) INFORMATION FOR SEQ ID NO:54:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 90 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

GATCCACTGA ACCTGGCTGG GACGCCGCTA GCCAGGTTAC TCGTGGCATA GATCCAGGGC	60
TTGGGAGCCT GGCCAGGTCT CTGTTGGTAC	90

(2) INFORMATION FOR SEQ ID NO:55:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

Gln	Gln	Arg	Pro	Gly	Gln	Ala	Pro	Lys	Pro	Trp	Ile	Tyr	Ala	Thr	Ser
1															15
Asn	Leu	Ala	Ser	Gly	Val	Pro	Ala	Arg	Phe	Ser					
											20				25

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 321 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence

(B) LOCATION: 1...321

(D) OTHER INFORMATION: F9HZLC 1-1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

GAA	ATA	GTA	CTG	ACA	CAG	TCT	CCA	GCC	ACC	CTG	TCT	TTG	TCT	CCA	GGG	48
Glu	Ile	Val	Leu	Thr	Gln	Ser	Pro	Ala	Thr	Leu	Ser	Leu	Ser	Pro	Gly	
1															15	

GAA	AGA	GCC	ACC	CTC	TCC	TGC	AGG	GCC	AGC	TCA	AGT	GTA	AAT	TAC	ATG	96
Glu	Arg	Ala	Thr	Leu	Ser	Cys	Arg	Ala	Ser	Ser	Ser	Val	Asn	Tyr	Met	
															20	
															25	
															30	

CAC	TGG	TAC	CAA	CAG	AGA	CCT	GGC	CAG	GCT	CCC	AAG	CCC	TGG	ATC	TAT	144
His	Trp	Tyr	Gln	Gln	Arg	Pro	Gly	Gln	Ala	Pro	Lys	Pro	Trp	Ile	Tyr	
															35	
															40	
															45	

GCC ACG AGT AAC CTG GCT AGC GGC GTC CCA GCC AGG TTC AGT GGA TCC	192		
Ala Thr Ser Asn Leu Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser			
50	55	60	
GGG TCT GGG ACA GAT TTC ACT CTC ACC ATC AGC AGT CTA GAG CCT GAA	240		
Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro Glu			
65	70	75	80
GAT TTT GCG GTT TAT TAC TGT CAG CAG TGG AGT ATT AAC CCG CGG ACG	288		
Asp Phe Ala Val Tyr Tyr Cys Gln Gln Trp Ser Ile Asn Pro Arg Thr			
85	90	95	
TTC GGC GGA GGG ACC AAG GTG GAG ATC AAA CGA	321		
Phe Gly Gly Thr Lys Val Glu Ile Lys Arg			
100	105		

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly			
1	5	10	15
His Trp Tyr Gln Gln Arg Pro Gly Gln Ala Pro Lys Pro Trp Ile Tyr			
35	40	45	
Ala Thr Ser Asn Leu Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser			
50	55	60	
Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro Glu			
65	70	75	80

Asp Phe Ala Val Tyr Tyr Cys Gln Gln Trp Ser Ile Asn Pro Arg Thr
 85 90 95
 Phe Gly Gly Thr Lys Val Glu Ile Lys Arg
 100 105

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

GATCCGGGTC TGGGACAGAT TACACTCTCA CGATATCCAG T

41

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

CTAGACTGGA TATCGTGAGA GTGTAATCTG TCCCAGACCC G

41

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser

1

5

10

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 321 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence

(B) LOCATION: 1...321

(D) OTHER INFORMATION: F9HZLC 1-2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

GAA ATA GTA CTG ACA CAG TCT CCA GCC ACC CTG TCT TTG TCT CCA GGG	48
Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly	
1 5 10 15	
GAA AGA GCC ACC CTC TCC TGC AGG GCC AGC TCA AGT GTA AAT TAC ATG	96
Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Ser Ser Val Asn Tyr Met	
20 25 30	
CAC TGG TAC CAA CAG AGA CCT GGC CAG GCT CCC AAG CCC TGG ATC TAT	144
His Trp Tyr Gln Gln Arg Pro Gly Gln Ala Pro Lys Pro Trp Ile Tyr	
35 40 45	
GCC ACG AGT AAC CTG GCT AGC GGC GTC CCA GCC AGG TTC AGT GGA TCC	192
Ala Thr Ser Asn Leu Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser	
50 55 60	
GGG TCT GGG ACA GAT TAC ACT CTC ACG ATA TCC AGT CTA GAG CCT GAA	240
Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Glu Pro Glu	
65 70 75 80	
GAT TTT GCG GTT TAT TAC TGT CAG CAG TGG AGT ATT AAC CCG CGG ACG	288
Asp Phe Ala Val Tyr Tyr Cys Gln Gln Trp Ser Ile Asn Pro Arg Thr	
85 90 95	
TTC GGC GGA GGG ACC AAG GTG GAG ATC AAA CGA	321
Phe Gly Gly Thr Lys Val Glu Ile Lys Arg	
100 105	

(2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
 1 5 10 15
 Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Ser Ser Val Asn Tyr Met
 20 25 30
 His Trp Tyr Gln Gln Arg Pro Gly Gln Ala Pro Lys Pro Trp Ile Tyr
 35 40 45
 Ala Thr Ser Asn Leu Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser
 50 55 60
 Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Glu Pro Glu
 65 70 75 80
 Asp Phe Ala Val Tyr Tyr Cys Gln Gln Trp Ser Ile Asn Pro Arg Thr
 85 90 95
 Phe Gly Gly Thr Lys Val Glu Ile Lys Arg
 100 105

(2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 165 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

AGTACTCACC CAGAGCCCAA GCAGCCTGAG CGCCAGCGTG GGTGACAGAG TGACCATCAC	60
CTGCAGGGCC AGCTCAAGTG TAAATTACAT GCACTGGTAC CAGCAGAAGC CAGGTAAGGC	120
TCCAAAGCCT TGGATCTACG CCACTAGTAA CCTGGCTTCT GGTGT	165

(2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 161 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

CCGCAGGTTA ATACTCCACT GCTGGCAGTA GTAGGTGGCG ATATCCTCTG GCTGGAGGCT	60
GCTGATGGTG AAGGTGTAGT CTGTACCGCT ACCGGATCCG CTGAATCTGC TTGGCACACC	120
AGAAGCCAGG TTACTAGTGG CGTAGATCCA AGGCTTTGGA G	161

(2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 280 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence

(B) LOCATION: 2...280

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

A	GTA	CTC	ACC	CAG	AGC	CCA	AGC	AGC	CTG	AGC	GCC	AGC	GTG	GGT	GAC	AGA	49
Val	Leu	Thr	Gln	Ser	Pro	Ser	Ser	Leu	Ser	Ala	Ser	Val	Gly	Asp	Arg		
1		5							10						15		
GTG ACC ATC ACC TGC AGG GCC AGC TCA AGT GTA AAT TAC ATG CAC TGG																97	
Val	Thr	Ile	Thr	Cys	Arg	Ala	Ser	Ser	Ser	Val	Asn	Tyr	Met	His	Trp		
20		25								30							
TAC CAG CAG AAG CCA GGT AAG GCT CCA AAG CCT TGG ATC TAC GCC ACT																145	
Tyr	Gln	Gln	Lys	Pro	Gly	Lys	Ala	Pro	Lys	Pro	Trp	Ile	Tyr	Ala	Thr		
35		40								45							
AGT AAC CTG GCT TCT GGT GTG CCA AGC AGA TTC AGC GGA TCC GGT AGC																193	
Ser	Asn	Leu	Ala	Ser	Gly	Val	Pro	Ser	Arg	Phe	Ser	Gly	Ser				
50		55							60								
GGT ACA GAC TAC ACC TTC ACC ATC AGC AGC CTC CAG CCA GAG GAT ATC																241	
Gly	Thr	Asp	Tyr	Thr	Phe	Thr	Ile	Ser	Ser	Leu	Gln	Pro	Glu	Asp	Ile		
65		70							75				80				
GCC ACC TAC TAC TGC CAG CAG TGG AGT ATT AAC CCG CGG																280	
Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	Trp	Ser	Ile	Asn	Pro	Arg					
85		90															

(2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 93 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE: internal
- (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

Val Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg
 1 5 10 15
 Val Thr Ile Thr Cys Arg Ala Ser Ser Ser Val Asn Tyr Met His Trp
 20 25 30
 Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Pro Trp Ile Tyr Ala Thr
 35 40 45
 Ser Asn Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser
 50 55 60
 Gly Thr Asp Tyr Thr Phe Thr Ile Ser Ser Leu Gln Pro Glu Asp Ile
 65 70 75 80
 Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ile Asn Pro Arg
 85 90

(2) INFORMATION FOR SEQ ID NO:67:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

TTTAGTACTC ACCCAGAGCC CAAGCAG

27

(2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

TTCCGCGGGT TAATACTCCA CTGCTGG

27

(2) INFORMATION FOR SEQ ID NO:69:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 33 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

CTCGAGGAGT ACTATCTGGG AGTGGACACC TGT

33

(2) INFORMATION FOR SEQ ID NO:70:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE: N-terminal
- (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

Arg Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala
1 5 10 15
Ala

(2) INFORMATION FOR SEQ ID NO:71:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

GGACGTTTCGG CCAAGGGACC AAGGTGGAAA TCAAACGGAC TGTGGCGG

48

(2) INFORMATION FOR SEQ ID NO:72:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

CGCCGCCACA GTCCGTTGA TTTCCACCTT GGTCCCTTGG CCGAACGTCC GC

52

(2) INFORMATION FOR SEQ ID NO:73:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 321 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 1...321
(D) OTHER INFORMATION: F9HZLC 2-0

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

CAG ATA GTA CTC ACC CAG AGC CCA AGC AGC CTG AGC GCC AGC GTG GGT 48
Gln Ile Val Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

GAC AGA GTG ACC ATC ACC TGC AGG GCC AGC TCA AGT GTA AAT TAC ATG	96
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Ser Ser Val Asn Tyr Met	
20 25 30	

CAC TGG TAC CAG CAG AAG CCA GGT AAG GCT CCA AAG CCT TGG ATC TAC 144
 His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Pro Trp Ile Tyr
 35 40 45

GCC ACT AGT AAC CTG GCT TCT GGT GTG CCA AGC AGA TTC AGC GGA TCC 192
 Ala Thr Ser Asn Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
 50 55 60

GGT AGC GGT ACA GAC TAC ACC TTC ACC ATC AGC AGC CTC CAG CCA GAG 240
 Gly Ser Gly Thr Asp Tyr Thr Phe Thr Ile Ser Ser Leu Gln Pro Glu
 65 70 75 80

GAT ATC GCC ACC TAC TAC TGC CAG CAG TGG AGT ATT AAC CCG CGG ACG
 Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ile Asn Pro Arg Thr
 85 90 95

288

TTC GGC CAA GGG ACC AAG GTG GAA ATC AAA CGG
 Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
 100 105

321

(2) INFORMATION FOR SEQ ID NO:74:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(iii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

Gln Ile Val Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1 5 10 15
 Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Ser Ser Val Asn Tyr Met
 20 25 30
 His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Pro Trp Ile Tyr
 35 40 45
 Ala Thr Ser Asn Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
 50 55 60
 Gly Ser Gly Thr Asp Tyr Thr Phe Thr Ile Ser Ser Leu Gln Pro Glu
 65 70 75 80
 Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ile Asn Pro Arg Thr
 85 90 95
 Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
 100 105

(2) INFORMATION FOR SEQ ID NO:75:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 94 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:
- (ix) FEATURE:
 - (A) NAME/KEY: Coding Sequence
 - (B) LOCATION: 27...94
 - (D) OTHER INFORMATION:

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

GAATTCTGAG CACACAGGAC CTCACC ATG GGA TGG AGC TGT ATC ATC CTC TTC	53
Met Gly Trp Ser Cys Ile Ile Leu Phe	
1	5

TTG GTA GCA ACA GCT ACA GGT GTC CAC TCC CAG ATA GTA CT	94
Leu Val Ala Thr Ala Thr Gly Val His Ser Gln Ile Val Leu	
10	15
	20

(2) INFORMATION FOR SEQ ID NO:76:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

Met	Gly	Trp	Ser	Cys	Ile	Ile	Leu	Phe	Leu	Val	Ala	Thr	Ala	Thr	Gly
1															15
Val His Ser Gln Ile Val Leu															
20															

(2) INFORMATION FOR SEQ ID NO:77:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 401 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence

(B) LOCATION: 27...401

(D) OTHER INFORMATION: F9HZLC 1-3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

GAATTCTGAG	CACACAGGAC	CTCACC	ATG	GGA	TGG	AGC	TGT	ATC	ATC	CTC	TTC	53
Met Gly Trp Ser Cys Ile Ile Leu Phe												
1												5

TTG	GTA	GCA	ACA	GCT	ACA	GGT	GTC	CAC	TCC	CAG	ATA	GTA	CTG	ACA	CAG	101
Leu Val Ala Thr Ala Thr Gly Val His Ser Gln Ile Val Leu Thr Gln																
10															25	

TCT CCA GCC ACC CTG TCT TTG TCT CCA GGG GAA AGA GCC ACC CTC TCC 149
 Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser
 30 35 40

TGC AGG GCC AGC TCA AGT GTA AAT TAC ATG CAC TGG TAC CAA CAG AGA 197
 Cys Arg Ala Ser Ser Ser Val Asn Tyr Met His Trp Tyr Gln Gln Arg
 45 50 55

CCT GGC CAG GCT CCC AAG CCC TGG ATC TAT GCC ACG AGT AAC CTG GCT 245
 Pro Gly Gln Ala Pro Lys Pro Trp Ile Tyr Ala Thr Ser Asn Leu Ala
 60 65 70

AGC GGC GTC CCA GCC AGG TTC AGT GGA TCC GGG TCT GGG ACA GAT TAC 293
 Ser Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Thr Asp Tyr
 75 80 85

ACT CTC ACG ATA TCC AGT CTA GAG CCT GAA GAT TTT GCG GTT TAT TAC 341
 Thr Leu Thr Ile Ser Ser Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr
 90 95 100 105

TGT CAG CAG TGG AGT ATT AAC CCG CGG ACG TTC GGC GGA GGG ACC AAG 389
 Cys Gln Gln Trp Ser Ile Asn Pro Arg Thr Phe Gly Gly Thr Lys
 110 115 120

GTG GAG ATC AAA 401
 Val Glu Ile Lys
 125

(2) INFORMATION FOR SEQ ID NO:78:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 125 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

Met	Gly	Trp	Ser	Cys	Ile	Ile	Leu	Phe	Leu	Val	Ala	Thr	Ala	Thr	Gly
1															15
Val	His	Ser	Gln	Ile	Val	Leu	Thr	Gln	Ser	Pro	Ala	Thr	Leu	Ser	Leu
				20				25						30	
Ser	Pro	Gly	Glu	Arg	Ala	Thr	Leu	Ser	Cys	Arg	Ala	Ser	Ser	Ser	Val
								35						45	
Asn	Tyr	Met	His	Trp	Tyr	Gln	Gln	Arg	Pro	Gly	Gln	Ala	Pro	Lys	Pro
				50				55						60	
Trp	Ile	Tyr	Ala	Thr	Ser	Asn	Leu	Ala	Ser	Gly	Val	Pro	Ala	Arg	Phe
	65				70				75					80	
Ser	Gly	Ser	Gly	Thr	Asp	Tyr	Thr	Leu	Thr	Ile	Ser	Ser	Leu		
					85			90					95		
Glu	Pro	Glu	Asp	Phe	Ala	Val	Tyr	Tyr	Cys	Gln	Gln	Trp	Ser	Ile	Asn
					100			105					110		
Pro	Arg	Thr	Phe	Gly	Gly	Gly	Thr	Lys	Val	Glu	Ile	Lys			
								115					125		

(2) INFORMATION FOR SEQ ID NO:79:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 81 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

AGGCCTCTGG	ATACACCTTC	ACTAACTATG	GAATGAACTG	GGTGCACAG	GCCCCTGGAC	60
AAGGGCTCGA	GTGGATGGGA	T				81

(2) INFORMATION FOR SEQ ID NO:80:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 99 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

TGTCTAGAGA GAAGACAAAC CGTCCTTGA AGTCATCAAC ATATGTTGAC TTTCCATTTC TGGTGTAT CCATCCATC CACTCGAGCC CTTGTCCAG	60 99
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(2) INFORMATION FOR SEQ ID NO:81:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 87 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

GGTTGTCTT CTCTCTAGAC ACCTCTGTCA GCACGGCATA TCTACAGATC AGCAGCCTAA AGGCTGAGGA CACTGCAGTG TATTCT	60 87
--	----------

(2) INFORMATION FOR SEQ ID NO:82:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 86 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

GGTACCCCTGG CCCCAGTAAG TAAAAGGGAA GTAACCATCC ATATTCCTT CTCTCGTACA 60
GAAATACACT GCAGTGTCCCT CAGCCT 86

(2) INFORMATION FOR SEQ ID NO:83:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 278 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence

(B) LOCATION: 3...278

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

AG GCC TCT GGA TAC ACC TTC ACT AAC TAT GGA ATG AAC TGG GTG CGA 47
Ala Ser Gly Tyr Thr Phe Thr Asn Tyr Gly Met Asn Trp Val Arg
1 5 10 15

CAG GCC CCT GGA CAA GGG CTC GAG TGG ATG GGA TGG ATA AAC ACC AGA 95
Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly Trp Ile Asn Thr Arg
20 25 30

AAT GGA AAG TCA ACA TAT GTT GAT GAC TTC AAG GGA CGG TTT GTC TTC	143	
Asn Gly Lys Ser Thr Tyr Val Asp Asp Phe Lys Gly Arg Phe Val Phe		
35	40	45
TCT CTA GAC ACC TCT GTC AGC ACG GCA TAT CTA CAG ATC AGC AGC CTA	191	
Ser Leu Asp Thr Ser Val Ser Thr Ala Tyr Leu Gln Ile Ser Ser Leu		
50	55	60
AAG GCT GAG GAC ACT GCA GTG TAT TTC TGT ACG AGA GAA GGG AAT ATG	239	
Lys Ala Glu Asp Thr Ala Val Tyr Phe Cys Thr Arg Glu Gly Asn Met		
65	70	75
GAT GGT TAC TTC CCT TTT ACT TAC TGG GGC CAG GGT ACC	278	
Asp Gly Tyr Phe Pro Phe Thr Tyr Trp Gly Gln Gly Thr		
80	85	90

(2) INFORMATION FOR SEQ ID NO:84:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 92 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

Ala Ser Gly Tyr Thr Phe Thr Asn Tyr Gly Met Asn Trp Val Arg Gln			
1	5	10	15
Ala Pro Gly Gln Gly Leu Glu Trp Met Gly Trp Ile Asn Thr Arg Asn			
20	25	30	
Gly Lys Ser Thr Tyr Val Asp Asp Phe Lys Gly Arg Phe Val Phe Ser			
35	40	45	
Leu Asp Thr Ser Val Ser Thr Ala Tyr Leu Gln Ile Ser Ser Leu Lys			
50	55	60	
Ala Glu Asp Thr Ala Val Tyr Phe Cys Thr Arg Glu Gly Asn Met Asp			
65	70	75	80

Gly Tyr Phe Pro Phe Thr Tyr Trp Gly Gln Gly Thr
85 90

(2) INFORMATION FOR SEQ ID NO:85:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

AGGCCTCTGG ATACACCTTC ACTAACTATG

30

(2) INFORMATION FOR SEQ ID NO:86:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

GGTACCCCTGG CCCCAGTAAG TAAAAG

26

(2) INFORMATION FOR SEQ ID NO:87:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

CCAGACTCGA CTAGTTGGAT CTGGGAGTGG ACACCTG

37

(2) INFORMATION FOR SEQ ID NO:88:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 446 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence

(B) LOCATION: 27...446

(D) OTHER INFORMATION: F9HZHC 3-0

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

GAATTCTGAG CACACAGGAC CTCACC ATG GGA TGG AGC TGT ATC ATC CTC TTC	53		
Met Gly Trp Ser Cys Ile Ile Leu Phe			
1	5		
TTG GTA GCA ACA GCT ACA GGT GTC CAC TCC CAG ATC CAA CTA GTG CAA	101		
Leu Val Ala Thr Ala Thr Gly Val His Ser Gln Ile Gln Leu Val Gln			
10	15	20	25
TCT GGG TCT GAG TTG AAG AAG CCT GGG GCC TCA GTG AAG GTT TCC TGC	149		
Ser Gly Ser Glu Leu Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys			
30	35	40	
AAG GCC TCT GGA TAC ACC TTC ACT AAC TAT GGA ATG AAC TGG GTG CGA	197		
Lys Ala Ser Gly Tyr Thr Phe Thr Asn Tyr Gly Met Asn Trp Val Arg			
45	50	55	
CAG GCC CCT GGA CAA GGG CTC GAG TGG ATG GGA TGG ATA AAC ACC AGA	245		
Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly Trp Ile Asn Thr Arg			
60	65	70	
AAT GGA AAG TCA ACA TAT GTT GAT GAC TTC AAG GGA CGG TTT GTC TTC	293		
Asn Gly Lys Ser Thr Tyr Val Asp Asp Phe Lys Gly Arg Phe Val Phe			
75	80	85	
TCT CTA GAC ACC TCT GTC AGC ACG GCA TAT CTA CAG ATC AGC AGC CTA	341		
Ser Leu Asp Thr Ser Val Ser Thr Ala Tyr Leu Gln Ile Ser Ser Leu			
90	95	100	105
AAG GCT GAG GAC ACT GCA GTG TAT TTC TGT ACG AGA GAA GGG AAT ATG	389		
Lys Ala Glu Asp Thr Ala Val Tyr Phe Cys Thr Arg Glu Gly Asn Met			
110	115	120	
GAT GGT TAC TTC CCT TTT ACT TAC TGG GGC CAG GGT ACC CTG GTC ACC	437		
Asp Gly Tyr Phe Pro Phe Thr Tyr Trp Gly Gln Gly Thr Leu Val Thr			
125	130	135	
GTC TCC TCT	446		
Val Ser Ser			
140			

(2) INFORMATION FOR SEQ ID NO:89:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 140 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

Met	Gly	Trp	Ser	Cys	Ile	Ile	Leu	Phe	Leu	Val	Ala	Thr	Ala	Thr	Gly
1					5					10				15	
Val	His	Ser	Gln	Ile	Gln	Leu	Val	Gln	Ser	Gly	Ser	Glu	Leu	Lys	Lys
					20				25				30		
Pro	Gly	Ala	Ser	Val	Lys	Val	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Phe
					35				40				45		
Thr	Asn	Tyr	Gly	Met	Asn	Trp	Val	Arg	Gln	Ala	Pro	Gly	Gln	Gly	Leu
					50				55				60		
Glu	Trp	Met	Gly	Trp	Ile	Asn	Thr	Arg	Asn	Gly	Lys	Ser	Thr	Tyr	Val
					65				70			75		80	
Asp	Asp	Phe	Lys	Gly	Arg	Phe	Val	Phe	Ser	Leu	Asp	Thr	Ser	Val	Ser
					85				90				95		
Thr	Ala	Tyr	Leu	Gln	Ile	Ser	Ser	Leu	Lys	Ala	Glu	Asp	Thr	Ala	Val
					100				105				110		
Tyr	Phe	Cys	Thr	Arg	Glu	Gly	Asn	Met	Asp	Gly	Tyr	Phe	Pro	Phe	Thr
					115				120				125		
Tyr	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser				
					130				135				140		

(2) INFORMATION FOR SEQ ID NO:90:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

AGTACTGACA CAGTCTCCAT CCTCCCTGTC TGCATCTGTT GGGGACAGAG TCACCATCAC	60
TTGCAGGGCC AGCTCAAGTG TAAATTACAT	90

- (2) INFORMATION FOR SEQ ID NO:91:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 108 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

CTTGATGGGA CGCCGCTAGC CAGGTTACTC GTGGCATAGA TCCAGGGCTT GGGAGCTTG	60
CCAGGTTCT GTGGTACCA GTGCATGTAA TTTACACTTG AGCTGGCC	108

- (2) INFORMATION FOR SEQ ID NO:92:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 108 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

TAACCTGGCT AGCGGCGTCC CATCAAGGTT CAGTGGATCC GGGTCTGGGA CAGATTACAC	60
TCTCACGATA TCCAGTCTAC AACCTGAAGA TTTTGCGACT TATTACTG	108

(2) INFORMATION FOR SEQ ID NO:93:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 102 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

GGCGCCGCCA CAGTCGTTT GATCTCCAGC TTGGTCCCTC CGCCGAACGT CCGCGGGTTA	60
ATACTCCACT GCTGACAGTA ATAAGTCGCA AAATCTTCAG GT	102

(2) INFORMATION FOR SEQ ID NO:94:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 330 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:
- (ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 2...328
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

A	GTA	CTG	ACA	CAG	TCT	CCA	TCC	TCC	CTG	TCT	GCA	TCT	GTT	GGG	GAC	AGA	49
Val	Leu	Thr	Gln	Ser	Pro	Ser	Ser	Leu	Ser	Ala	Ser	Val	Gly	Asp	Arg		
1															15		
GTC	ACC	ATC	ACT	TGC	AGG	GCC	AGC	TCA	AGT	GTA	AAT	TAC	ATG	CAC	TGG	97	
Val	Thr	Ile	Thr	Cys	Arg	Ala	Ser	Ser	Ser	Val	Asn	Tyr	Met	His	Trp		
20															30		
TAC	CAA	CAG	AAA	CCT	GGC	AAA	GCT	CCC	AAG	CCC	TGG	ATC	TAT	GCC	ACG	145	
Tyr	Gln	Gln	Lys	Pro	Gly	Lys	Ala	Pro	Lys	Pro	Trp	Ile	Tyr	Ala	Thr		
35															45		
AGT	AAC	CTG	GCT	AGC	GGC	GTC	CCA	TCA	AGG	TTC	AGT	GGA	TCC	GGG	TCT	193	
Ser	Asn	Leu	Ala	Ser	Gly	Val	Pro	Ser	Arg	Phe	Ser	Gly	Ser	Gly	Ser		
50															60		
GGG	ACA	GAT	TAC	ACT	CTC	ACG	ATA	TCC	AGT	CTA	CAA	CCT	GAA	GAT	TTT	241	
Gly	Thr	Asp	Tyr	Thr	Leu	Thr	Ile	Ser	Ser	Leu	Gln	Pro	Glu	Asp	Phe		
65															80		
GCG	ACT	TAT	TAC	TGT	CAG	CAG	TGG	AGT	ATT	AAC	CCG	CGG	ACG	TTC	GGC	289	
Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	Trp	Ser	Ile	Asn	Pro	Arg	Thr	Phe	Gly		
85															95		
GGA	GGG	ACC	AAG	CTG	GAG	ATC	AAA	CGA	ACT	GTG	GCG	GCG	CC		330		
Gly	Gly	Thr	Lys	Leu	Glu	Ile	Lys	Arg	Thr	Val	Ala	Ala					
100																	

(2) INFORMATION FOR SEQ ID NO:95:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 109 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE: internal
- (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

Val	Leu	Thr	Gln	Ser	Pro	Ser	Ser	Leu	Ser	Ala	Ser	Val	Gly	Asp	Arg
1					5				10					15	
Val	Thr	Ile	Thr	Cys	Arg	Ala	Ser	Ser	Ser	Val	Asn	Tyr	Met	His	Trp
					20				25					30	
Tyr	Gln	Gln	Lys	Pro	Gly	Lys	Ala	Pro	Lys	Pro	Trp	Ile	Tyr	Ala	Thr
					35				40					45	
Ser	Asn	Leu	Ala	Ser	Gly	Val	Pro	Ser	Arg	Phe	Ser	Gly	Ser		
					50			55			60				
Gly	Thr	Asp	Tyr	Thr	Leu	Thr	Ile	Ser	Ser	Leu	Gln	Pro	Glu	Asp	Phe
					65			70			75			80	
Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	Trp	Ser	Ile	Asn	Pro	Arg	Thr	Phe	Gly
					85				90					95	
Gly	Gly	Thr	Lys	Leu	Glu	Ile	Lys	Arg	Thr	Val	Ala	Ala			
					100				105						

(2) INFORMATION FOR SEQ ID NO:96:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 26 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

CAAGTACTGA CACAGTCTCC ATCCTC

26

(2) INFORMATION FOR SEQ ID NO:97:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

AGGGCGCCGC CACAGTTCGT TTGATC

26

(2) INFORMATION FOR SEQ ID NO:98:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 412 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence

(B) LOCATION: 27...412

(D) OTHER INFORMATION: F9HZLC 3-0

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

GAATTCTGAG CACACAGGAC CTCACC ATG GGA TGG AGC TGT ATC ATC CTC TTC	53		
Met Gly Trp Ser Cys Ile Ile Leu Phe			
1	5		
TTG GTA GCA ACA GCT ACA GGT GTC CAC TCC CAG ATA GTA CTG ACA CAG	101		
Leu Val Ala Thr Ala Thr Gly Val His Ser Gln Ile Val Leu Thr Gln			
10	15	20	25
TCT CCA TCC TCC CTG TCT GCA TCT GTT GGG GAC AGA GTC ACC ATC ACT	149		
Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr			
30	35	40	
TGC AGG GCC AGC TCA AGT GTA AAT TAC ATG CAC TGG TAC CAA CAG AAA	197		
Cys Arg Ala Ser Ser Ser Val Asn Tyr Met His Trp Tyr Gln Gln Lys			
45	50	55	
CCT GGC AAA GCT CCC AAG CCC TGG ATC TAT GCC ACG AGT AAC CTG GCT	245		
Pro Gly Lys Ala Pro Lys Pro Trp Ile Tyr Ala Thr Ser Asn Leu Ala			
60	65	70	
AGC GGC GTC CCA TCA AGG TTC AGT GGA TCC GGG TCT GGG ACA GAT TAC	293		
Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Thr Asp Tyr			
75	80	85	
ACT CTC ACG ATA TCC AGT CTA CAA CCT GAA GAT TTT GCG ACT TAT TAC	341		
Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr			
90	95	100	105
TGT CAG CAG TGG AGT ATT AAC CCG CGG ACG TTC GGC GGA GGG ACC AAG	389		
Cys Gln Gln Trp Ser Ile Asn Pro Arg Thr Phe Gly Gly Thr Lys			
110	115	120	
CTG GAG ATC AAA CGA ACT GTG GC	412		
Leu Glu Ile Lys Arg Thr Val Val			
125			

(2) INFORMATION FOR SEQ ID NO:99:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

Met	Gly	Trp	Ser	Cys	Ile	Ile	Leu	Phe	Leu	Val	Ala	Thr	Ala	Thr	Gly
1					5					10				15	
Val	His	Ser	Gln	Ile	Val	Leu	Thr	Gln	Ser	Pro	Ser	Ser	Leu	Ser	Ala
					20				25				30		
Ser	Val	Gly	Asp	Arg	Val	Thr	Ile	Thr	Cys	Arg	Ala	Ser	Ser	Ser	Val
					35			40				45			
Asn	Tyr	Met	His	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Lys	Ala	Pro	Lys	Pro
					50			55			60				
Trp	Ile	Tyr	Ala	Thr	Ser	Asn	Leu	Ala	Ser	Gly	Val	Pro	Ser	Arg	Phe
					65			70			75			80	
Ser	Gly	Ser	Gly	Thr	Asp	Tyr	Thr	Leu	Thr	Ile	Ser	Ser	Leu		
					85			90			95				
Gln	Pro	Glu	Asp	Phe	Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	Trp	Ser	Ile	Asn
					100			105			110				
Pro	Arg	Thr	Phe	Gly	Gly	Gly	Thr	Lys	Leu	Glu	Ile	Lys	Arg	Thr	Val
					115			120			125				
Val															

(2) INFORMATION FOR SEQ ID NO:100:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

CAAATAGTAC TCTCCCAGTC TCCAGC

26

(2) INFORMATION FOR SEQ ID NO:101:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 41 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

GGATAAGCTT GGCGCCGCAA CAGTCGGTTT GATTTCAGC T

41

(2) INFORMATION FOR SEQ ID NO:102:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 335 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:
- (ix) FEATURE:

127

(A) NAME/KEY: Coding Sequence
 (B) LOCATION: 1...335
 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

CAG ATA GTA CTC TCC CAG TCT CCA GCA ATC CTG TCT GCA TCT CCA GGG	48
Gln Ile Val Leu Ser Gln Ser Pro Ala Ile Leu Ser Ala Ser Pro Gly	
1 5 10 15	
GAG AAG GTC ACA ATG ACT TGC AGG GCC AGC TCA AGT GTA AAT TAC ATG	96
Glu Lys Val Thr Met Thr Cys Arg Ala Ser Ser Ser Val Asn Tyr Met	
20 25 30	
CAC TGG TAC CAG CAG AAG CCA GGA TCC TCC CCC AAA CCC TGG ATT TAT	144
His Trp Tyr Gln Gln Lys Pro Gly Ser Ser Pro Lys Pro Trp Ile Tyr	
35 40 45	
GCC ACA TCC AAC CTG GCT TCT GGA GTC CCT GCT CGC TTC AGT GGC AGT	192
Ala Thr Ser Asn Leu Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser	
50 55 60	
GGG TCT GGG ACC TCT TAC TCT CTC ACA ATC AGC AGA GTG GAG GCT GAA	240
Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Arg Val Glu Ala Glu	
65 70 75 80	
GAT GCT GCC ACT TAT TAC TGC CAG CAG TGG AGT ATT AAC CCA CGG ACG	288
Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ile Asn Pro Arg Thr	
85 90 95	
TTC GGT GGA GGC ACC AAG CTG GAA ATC AAA CGG ACT GTT GCG GCG CC	335
Phe Gly Gly Thr Lys Leu Glu Ile Lys Arg Thr Val Ala Ala Pro	
100 105 110	

(2) INFORMATION FOR SEQ ID NO:103:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 112 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

Gln	Ile	Val	Leu	Ser	Gln	Ser	Pro	Ala	Ile	Leu	Ser	Ala	Ser	Pro	Gly
1					5				10					15	
Glu	Lys	Val	Thr	Met	Thr	Cys	Arg	Ala	Ser	Ser	Ser	Val	Asn	Tyr	Met
					20				25				30		
His	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Ser	Ser	Pro	Lys	Pro	Trp	Ile	Tyr
					35				40			45			
Ala	Thr	Ser	Asn	Leu	Ala	Ser	Gly	Val	Pro	Ala	Arg	Phe	Ser	Gly	Ser
					50				55			60			
Gly	Ser	Gly	Thr	Ser	Tyr	Ser	Leu	Thr	Ile	Ser	Arg	Val	Glu	Ala	Glu
					65				70			75		80	
Asp	Ala	Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	Trp	Ser	Ile	Asn	Pro	Arg	Thr
					85				90			95			
Phe	Gly	Gly	Gly	Thr	Lys	Leu	Glu	Ile	Lys	Arg	Thr	Val	Ala	Ala	Pro
					100				105			110			

(2) INFORMATION FOR SEQ ID NO:104:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 318 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence

(B) LOCATION: 1...318

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

CAG ATA GTA CTC TCC CAG TCT CCA GCA ATC CTG TCT GCA TCT CCA GGG	48
Gln Ile Val Leu Ser Gln Ser Pro Ala Ile Leu Ser Ala Ser Pro Gly	
1 5 10 15	
GAG AAG GTC ACA ATG ACT TGC AGG GCC AGC TCA AGT GTA AAT TAC ATG	96
Glu Lys Val Thr Met Thr Cys Arg Ala Ser Ser Ser Val Asn Tyr Met	
20 25 30	
CAC TGG TAC CAG CAG AAG CCA GGA TCC TCC CCC AAA CCC TGG ATT TAT	144
His Trp Tyr Gln Gln Lys Pro Gly Ser Ser Pro Lys Pro Trp Ile Tyr	
35 40 45	
GCC ACA TCC AAC CTG GCT TCT GGA GTC CCT GCT CGC TTC AGT GGC AGT	192
Ala Thr Ser Asn Leu Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser	
50 55 60	
GGG TCT GGG ACC TCT TAC TCT CTC ACA ATC AGC AGA GTG GAG GCT GAA	240
Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Arg Val Glu Ala Glu	
65 70 75 80	
GAT GCT GCC ACT TAT TAC TGC CAG CAG TGG AGT ATT AAC CCA CGG ACG	288
Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ile Asn Pro Arg Thr	
85 90 95	
TTC GGT GGA GGC ACC AAG CTG GAA ATC AAA	318
Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys	
100 105	

(2) INFORMATION FOR SEQ ID NO:105:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 106 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE: internal
- (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

Gln	Ile	Val	Leu	Ser	Gln	Ser	Pro	Ala	Ile	Leu	Ser	Ala	Ser	Pro	Gly
1					5				10					15	
Glu	Lys	Val	Thr	Met	Thr	Cys	Arg	Ala	Ser	Ser	Ser	Val	Asn	Tyr	Met
				20					25				30		
His	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Ser	Ser	Pro	Lys	Pro	Trp	Ile	Tyr
						35		40				45			
Ala	Thr	Ser	Asn	Leu	Ala	Ser	Gly	Val	Pro	Ala	Arg	Phe	Ser	Gly	Ser
			50			55				60					
Gly	Ser	Gly	Thr	Ser	Tyr	Ser	Leu	Thr	Ile	Ser	Arg	Val	Glu	Ala	Glu
			65			70			75				80		
Asp	Ala	Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	Trp	Ser	Ile	Asn	Pro	Arg	Thr
				85					90				95		
Phe	Gly	Gly	Gly	Thr	Lys	Leu	Glu	Ile	Lys						
				100			105								

(2) INFORMATION FOR SEQ ID NO:106:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

CAGATCCAAC TAGTGCAGTC TGGACCTGAG

30

(2) INFORMATION FOR SEQ ID NO:107:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

TTAAGCTTGC TAGCTGCAGA GACAGTGACC AG

32

(2) INFORMATION FOR SEQ ID NO:108:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 369 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence

(B) LOCATION: 1...369

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

CAG ATC CAA CTA GTG CAG TCT GGA CCT GAG CTG AAG AAG CCT GGA GAG	48
Gln Ile Gln Leu Val Gln Ser Gly Pro Glu Leu Lys Lys Pro Gly Glu	
1 5 10 15	
ACA GTC AAG ATC TCC TGC AAG GCT TCT GGG TAC ACC TTC ACA AAC TAT	96
Thr Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn Tyr	
20 25 30	
GGA ATG AAC TGG GTG AAG CAG GCT CCA GGA AAG GGT TTA AAG TGG ATG	144
Gly Met Asn Trp Val Lys Gln Ala Pro Gly Lys Gly Leu Lys Trp Met	
35 40 45	
GGC TGG ATA AAC ACC AGA AAT GGA AAG TCA ACA TAT GTT GAT GAC TTC	192
Gly Trp Ile Asn Thr Arg Asn Gly Lys Ser Thr Tyr Val Asp Asp Phe	
50 55 60	
AAG GGA CGG TTT GCC TTC TCT TTG GAA AGC TCT GCC AGC ACT GCC AAT	240
Lys Gly Arg Phe Ala Phe Ser Leu Glu Ser Ser Ala Ser Thr Ala Asn	
65 70 75 80	
TTG CAG ATC GAC AAC CTC AAA GAT GAG GAC ACG GCT ACA TAT TTC TGT	288
Leu Gln Ile Asp Asn Leu Lys Asp Glu Asp Thr Ala Thr Tyr Phe Cys	
85 90 95	
ACA AGA GAA GGG AAT ATG GAT GGT TAC TTC CCT TTT ACT TAC TGG GGC	336
Thr Arg Glu Gly Asn Met Asp Gly Tyr Phe Pro Phe Thr Tyr Trp Gly	
100 105 110	
CAA GGG ACT CTG GTC ACT GTC TCT GCA GCT AGC	369
Gln Gly Thr Leu Val Thr Val Ser Ala Ala Ser	
115 120	

(2) INFORMATION FOR SEQ ID NO:109:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 123 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE: internal
- (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

Gln	Ile	Gln	Leu	Val	Gln	Ser	Gly	Pro	Glu	Leu	Lys	Lys	Pro	Gly	Glu	
1					5				10					15		
Thr	Val	Lys	Ile	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Phe	Thr	Asn	Tyr	
					20				25					30		
Gly	Met	Asn	Trp	Val	Lys	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Lys	Trp	Met	
					35				40					45		
Gly	Trp	Ile	Asn	Thr	Arg	Asn	Gly	Lys	Ser	Thr	Tyr	Val	Asp	Asp	Phe	
					50				55					60		
Lys	Gly	Arg	Phe	Ala	Phe	Ser	Leu	Glu	Ser	Ser	Ala	Ser	Thr	Ala	Asn	
					65				70					75		80
Leu	Gln	Ile	Asp	Asn	Leu	Lys	Asp	Glu	Asp	Thr	Ala	Thr	Tyr	Phe	Cys	
					85				90					95		
Thr	Arg	Glu	Gly	Asn	Met	Asp	Gly	Tyr	Phe	Pro	Phe	Thr	Tyr	Trp	Gly	
					100				105					110		
Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ala	Ala	Ser						
					115				120							

(2) INFORMATION FOR SEQ ID NO:110:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 363 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:
- (ix) FEATURE:
 - (A) NAME/KEY: Coding Sequence
 - (B) LOCATION: 1...363

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

CAG ATC CAA CTA GTG CAG TCT GGA CCT GAG CTG AAG AAG CCT GGA GAG	48
Gln Ile Gln Leu Val Gln Ser Gly Pro Glu Leu Lys Lys Pro Gly Glu	
1 5 10 15	
ACA GTC AAG ATC TCC TGC AAG GCT TCT GGG TAC ACC TTC ACA AAC TAT	96
Thr Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn Tyr	
20 25 30	
GGA ATG AAC TGG GTG AAG CAG GCT CCA GGA AAG GGT TTA AAG TGG ATG	144
Gly Met Asn Trp Val Lys Gln Ala Pro Gly Lys Gly Leu Lys Trp Met	
35 40 45	
GGC TGG ATA AAC ACC AGA AAT GGA AAG TCA ACA TAT GTT GAT GAC TTC	192
Gly Trp Ile Asn Thr Arg Asn Gly Lys Ser Thr Tyr Val Asp Asp Phe	
50 55 60	
AAG GGA CGG TTT GCC TTC TCT TTG GAA AGC TCT GCC AGC ACT GCC AAT	240
Lys Gly Arg Phe Ala Phe Ser Leu Glu Ser Ser Ala Ser Thr Ala Asn	
65 70 75 80	
TTG CAG ATC GAC AAC CTC AAA GAT GAG GAC ACG GCT ACA TAT TTC TGT	288
Leu Gln Ile Asp Asn Leu Lys Asp Glu Asp Thr Ala Thr Tyr Phe Cys	
85 90 95	
ACA AGA GAA GGG AAT ATG GAT GGT TAC TTC CCT TTT ACT TAC TGG GGC	336
Thr Arg Glu Gly Asn Met Asp Gly Tyr Phe Pro Phe Thr Tyr Trp Gly	
100 105 110	
CAA GGG ACT CTG GTC ACT GTC TCT GCA	363
Gln Gly Thr Leu Val Thr Val Ser Ala	
115 120	

(2) INFORMATION FOR SEQ ID NO:111:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 121 amino acids
- (B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

Gln Ile Gln Leu Val Gln Ser Gly Pro Glu Leu Lys Lys Pro Gly Glu
1 5 10 15
Thr Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn Tyr
20 25 30
Gly Met Asn Trp Val Lys Gln Ala Pro Gly Lys Gly Leu Lys Trp Met
35 40 45
Gly Trp Ile Asn Thr Arg Asn Gly Lys Ser Thr Tyr Val Asp Asp Phe
50 55 60
Lys Gly Arg Phe Ala Phe Ser Leu Glu Ser Ser Ala Ser Thr Ala Asn
65 70 75 80
Leu Gln Ile Asp Asn Leu Lys Asp Glu Asp Thr Ala Thr Tyr Phe Cys
85 90 95
Thr Arg Glu Gly Asn Met Asp Gly Tyr Phe Pro Phe Thr Tyr Trp Gly
100 105 110
Gln Gly Thr Leu Val Thr Val Ser Ala
115 120